RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/564,823_
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IFWP

RAW SEQUENCE LISTING   DATE: 01/30/2006
PATENT APPLICATION: US/10/564,823   TIME: 15:08:36

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    3 <110> APPLICANT: Stein, Ulrike
    4         Schwabe, Holger
    5         Walther, Wolfgang
    6         Schlag, Peter Michael
    8 <120> TITLE OF INVENTION: 7a/5 Prognostin and its Use for the Diagnostics and Therapy
of
    9         Tumors
   11 <130> FILE REFERENCE: 2958-135
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/564,823
C--> 13 <141> CURRENT FILING DATE: 2006-01-18
   13 <150> PRIOR APPLICATION NUMBER: DE 103 32 854.8
   14 <151> PRIOR FILING DATE: 2003-07-18
   16 <150> PRIOR APPLICATION NUMBER: PCT/EP04/008053
   17 <151> PRIOR FILING DATE: 2004-07-19
   19 <160> NUMBER OF SEQ ID NOS: 8
   21 <170> SOFTWARE: PatentIn version 3.3
   23 <210> SEQ ID NO: 1
   24 <211> LENGTH: 2559
   25 <212> TYPE: DNA
   26 <213> ORGANISM: Homo sapiens
   28 <400> SEQUENCE: 1
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   33 caggacccag acttgcttca caattggccg gatgctttca cccttcgtgg taataatgct     180
   35 tccaaagttg caaatccatt ctggaatcaa ctgtctgctt ctaacccatt tttggatgac     240
   37 ataactcaac taagaaataa caggaagaga aataatattt ccatcttaaa ggaagatcct     300
   39 tttcttttct gtagagaaat agaaaatgga aattcttttg attcctccgg tgatgaactt     360
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   49 agccctggat gggcccagac acaacttgcg gaggtcacca tagcttgcaa agtaaaccat     660
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   53 gtggctgtgg gagaattcca agaggtgtct ctaagggctt ccttgatcc gccacacatg     780
   55 cttaaccatg atctttcgtg cactgtgagc ccgttgttgg aaatcatgtt aggcaacctc     840
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   67 catcccagtt ttactgttgt tttaacagtt tgtggacaca attatatgcc aggacagctt    1200
   69 acaatttctg atattaagaa gggtggaaaa aacatatctc cagttgtgtt tcagctctgg    1260
   71 gggaagcagt catttttact tgacaagcca caagatttaa gtatttctat tttttcctgt    1320
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 83 cctacatttc aagataaaac attgaacttt agcaactatg gggtaaccct gaaggcagtg  1680
 85 ctaagacaaa gcaagattga ttacttcctt gaatatttca aggggacac aatagctctc  1740
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 93 ctgcctttaa aaaaattgac ttatatctac tcagttgtat taaccttggt gtcagaaaaa  1980
 95 gtttatgatt ggaaagtttt agctgatgtc ctgggttact cacatctgtc cctggaagat  2040
 97 tttgatcaaa ttcaagcaga caaagaatca gagaaagttt cttatgttat aaagaagtta  2100
 99 aaggaagatt gccacacaga gagaaataca aggaagtttc tgtatgaact tattgtggct  2160
101 cttctgaaaa tggattgcca agagttagtc gcacgtctca tccaagaagc tgctgttctg  2220
103 acttcagctg tcaagcttgg aaaaggctgg agggaactag ctgaaaagtt agtacgactc  2280
105 acaaagcaac aaatggaggc atatgaaatt cctcatcgag gaaacactgg agatgttgct  2340
107 gttgagatga tgtggaaacc tgcctatgat tttctgtata cctggagtgc tcactatgga  2400
109 aataactaca gagatgtgtt acaagacctt cagtcagctt tggacagaat gaaaaaccct  2460
111 gtgactaaac actggagaga attaactgga gttttaatac tagtaaattc tttggaggtt  2520
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117 <211> LENGTH: 852
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
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128             20                  25                  30
131 Lys Ser Cys Asn Ile Thr Glu Cys Gln Asp Pro Asp Leu Leu His Asn
132         35                  40                  45
135 Trp Pro Asp Ala Phe Thr Leu Arg Gly Asn Asn Ala Ser Lys Val Ala
136     50                  55                  60
139 Asn Pro Phe Trp Asn Gln Leu Ser Ala Ser Asn Pro Phe Leu Asp Asp
140 65                  70                  75                  80
143 Ile Thr Gln Leu Arg Asn Asn Arg Lys Arg Asn Asn Ile Ser Ile Leu
144             85                  90                  95
147 Lys Glu Asp Pro Phe Leu Phe Cys Arg Glu Ile Glu Asn Gly Asn Ser
148             100                 105                 110
151 Phe Asp Ser Ser Gly Asp Glu Leu Asp Val His Gln Leu Leu Arg Gln
152         115                 120                 125
155 Thr Ser Ser Arg Asn Ser Gly Arg Ser Lys Ser Val Ser Glu Leu Leu
156     130                 135                 140
159 Asp Ile Leu Asp Asp Thr Ala His Ala His Gln Ser Ile His Asn Ser
160 145                 150                 155                 160
163 Asp Gln Ile Leu Leu His Asp Leu Glu Trp Leu Lys Asn Asp Arg Glu
164             165                 170                 175
167 Ala Tyr Lys Met Ala Trp Leu Ser Gln Arg Gln Leu Ala Arg Ser Cys
168             180                 185                 190
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171 Leu Asp Leu Asn Thr Ile Ser Gln Ser Pro Gly Trp Ala Gln Thr Gln
172         195                 200             205
175 Leu Ala Glu Val Thr Ile Ala Cys Lys Val Asn His Gln Gly Gly Ser
176         210                 215             220
179 Val Gln Leu Pro Glu Ser Asp Ile Thr Val His Val Pro Gln Gly His
180 225                 230                 235                 240
183 Val Ala Val Gly Glu Phe Gln Glu Val Ser Leu Arg Ala Phe Leu Asp
184             245                 250                 255
187 Pro Pro His Met Leu Asn His Asp Leu Ser Cys Thr Val Ser Pro Leu
188         260                 265             270
191 Leu Glu Ile Met Leu Gly Asn Leu Asn Thr Met Glu Ala Leu Leu Leu
192         275                 280             285
195 Glu Met Lys Ile Gly Ala Glu Val Arg Lys Asp Pro Phe Ser Gln Val
196         290                 295             300
199 Met Thr Glu Met Val Cys Leu His Ser Leu Gly Lys Glu Gly Pro Phe
200 305                 310             315                 320
203 Lys Val Leu Ser Asn Cys Tyr Ile Tyr Lys Asp Thr Ile Gln Val Lys
204             325                 330                 335
207 Leu Ile Asp Leu Ser Gln Val Met Tyr Leu Val Val Ala Ala Gln Ala
208         340                 345             350
211 Lys Ala Leu Pro Ser Pro Ala Ala Thr Ile Trp Asp Tyr Ile His Lys
212         355                 360                 365
215 Thr Thr Ser Ile Gly Ile Tyr Gly Pro Lys Tyr Ile His Pro Ser Phe
216         370                 375                 380
219 Thr Val Val Leu Thr Val Cys Gly His Asn Tyr Met Pro Gly Gln Leu
220 385                 390                 395                 400
223 Thr Ile Ser Asp Ile Lys Lys Gly Gly Lys Asn Ile Ser Pro Val Val
224             405                 410                 415
227 Phe Gln Leu Trp Gly Lys Gln Ser Phe Leu Leu Asp Lys Pro Gln Asp
228         420                 425                 430
231 Leu Ser Ile Ser Ile Phe Ser Cys Asp Pro Asp Phe Glu Val Lys Thr
232         435                 440                 445
235 Glu Gly Glu Arg Lys Glu Ile Lys Gln Lys Gln Leu Glu Ala Gly Glu
236         450                 455             460
239 Val Val His Gln Gln Phe Leu Phe Ser Leu Val Glu His Arg Glu Met
240 465                 470                 475                 480
243 His Leu Phe Asp Phe Cys Val Gln Val Glu Pro Pro Asn Gly Glu Pro
244             485                 490                 495
247 Val Ala Gln Phe Ser Ile Thr Thr Pro Asp Pro Thr Pro Asn Leu Lys
248         500                 505             510
251 Arg Leu Ser Asn Leu Pro Gly Tyr Leu Gln Lys Lys Glu Glu Ile Lys
252         515                 520             525
255 Ser Ala Pro Leu Ser Pro Lys Ile Leu Val Lys Tyr Pro Thr Phe Gln
256         530                 535             540
259 Asp Lys Thr Leu Asn Phe Ser Asn Tyr Gly Val Thr Leu Lys Ala Val
260 545                 550                 555                 560
263 Leu Arg Gln Ser Lys Ile Asp Tyr Phe Leu Glu Tyr Phe Lys Gly Asp
264             565                 570                 575
267 Thr Ile Ala Leu Leu Gly Glu Gly Lys Val Lys Ala Ile Gly Gln Ser
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268             580                 585                 590
271 Lys Val Lys Glu Trp Tyr Val Gly Val Leu Arg Gly Lys Ile Gly Leu
272         595                 600                 605
275 Val His Cys Lys Asn Val Lys Val Ile Ser Lys Glu Gln Val Met Phe
276     610                 615                 620
279 Met Ser Asp Ser Val Phe Thr Thr Arg Asn Leu Leu Glu Gln Ile Val
280 625                 630                 635                 640
283 Leu Pro Leu Lys Lys Leu Thr Tyr Ile Tyr Ser Val Val Leu Thr Leu
284             645                 650                 655
287 Val Ser Glu Lys Val Tyr Asp Trp Lys Val Leu Ala Asp Val Leu Gly
288             660                 665                 670
291 Tyr Ser His Leu Ser Leu Glu Asp Phe Asp Gln Ile Gln Ala Asp Lys
292         675                 680                 685
295 Glu Ser Glu Lys Val Ser Tyr Val Ile Lys Lys Leu Lys Glu Asp Cys
296     690                 695                 700
299 His Thr Glu Arg Asn Thr Arg Lys Phe Leu Tyr Glu Leu Ile Val Ala
300 705             710                 715                 720
303 Leu Leu Lys Met Asp Cys Gln Glu Leu Val Ala Arg Leu Ile Gln Glu
304             725                 730                 735
307 Ala Ala Val Leu Thr Ser Ala Val Lys Leu Gly Lys Gly Trp Arg Glu
308             740                 745                 750
311 Leu Ala Glu Lys Leu Val Arg Leu Thr Lys Gln Gln Met Glu Ala Tyr
312         755                 760                 765
315 Glu Ile Pro His Arg Gly Asn Thr Gly Asp Val Ala Val Glu Met Met
316     770                 775                 780
319 Trp Lys Pro Ala Tyr Asp Phe Leu Tyr Thr Trp Ser Ala His Tyr Gly
320 785             790                 795                 800
323 Asn Asn Tyr Arg Asp Val Leu Gln Asp Leu Gln Ser Ala Leu Asp Arg
324             805                 810                 815
327 Met Lys Asn Pro Val Thr Lys His Trp Arg Glu Leu Thr Gly Val Leu
328             820                 825                 830
331 Ile Leu Val Asn Ser Leu Glu Val Leu Arg Val Thr Ala Phe Ser Thr
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335 Ser Glu Glu Val
336     850
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342 <213> ORGANISM: Homo sapiens
344 <400> SEQUENCE: 3
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349 <211> LENGTH: 20
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351 <213> ORGANISM: Homo sapiens
353 <400> SEQUENCE: 4
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357 <210> SEQ ID NO: 5
358 <211> LENGTH: 32
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360 <213> ORGANISM: Homo sapiens
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366 <210> SEQ ID NO: 6
367 <211> LENGTH: 32
368 <212> TYPE: DNA
369 <213> ORGANISM: Homo sapiens
371 <400> SEQUENCE: 6
372 agtgtttcag aacttctgga cattttagac ga   32
375 <210> SEQ ID NO: 7
376 <211> LENGTH: 21
377 <212> TYPE: DNA
378 <213> ORGANISM: Homo sapiens
380 <400> SEQUENCE: 7
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384 <210> SEQ ID NO: 8
385 <211> LENGTH: 18
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo sapiens
389 <400> SEQUENCE: 8
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392 1   5   10   15
395 Trp Arg

VERIFICATION SUMMARY   DATE: 01/30/2006
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